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Attorney Docket No. DIVER1260-3

X CONTINUATION
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Box Patent Application
Assistant Commissioner for Patents
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Sir:

Transmitted herewith for filing is the **continuation** patent application of

Inventor(s): Jay M. Short; Barry Marrs; Jeffrey L. Stein

For: **PROTEIN ACTIVITY SCREENING OF CLONES HAVING DNA FROM UNCULTIVATED MICROORGANISMS**

This is a request for filing a **continuation** application under 37 C.F.R. 1.53(b), of prior U.S. application Serial No. 08/988,224; filed on December 10, 1997, now pending.

Enclosed are:

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Specification	34
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Filing fee to be charged to Deposit Account No. 07-1895 in amount of 380.00

This application claims priority under 35 U.S.C. § 120 to U.S. Patent Application Serial No. 08/988,224, filed December 10, 1997, which is a divisional of U.S. Patent Application Serial No. 08/657,409, filed June 3, 1996, which is a continuation-in-part of U.S. Patent Application Serial No. 08/568,994, filed December 7, 1995 (now abandoned), which is a continuation-in-part of U.S. Patent Application Serial No. 08/503,606, filed July 18, 1995, the contents of which are incorporated by reference in their entirety herein.

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104703-156667

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No payment of the issue fee, abandonment of, or termination of proceeding has occurred in the above-identified prior application.

1. ___ Cancel in this application original claim(s) _____.

2. ____ A preliminary amendment is enclosed.

The filing fee has been calculated as shown below:

For	Number Filed		Number Extra		Rate			Fee	
					Small Entity	Other Entity		Small Entity	Other Entity
Total Claims	3	=	0	X	$9	$18	=	$.000	$ .00
Independent Claims	2	=	0	X	$39	$78	=	$.000	0
Multiple Dependent Claims Presented: ___ Yes _X_ No					$130	$260			0
				BASIC FEE	$380	$760		$.00	$ 760.00
					TOTAL FEE			$380.00	$0.00

3. _X_ Please charge my Deposit Account No. 07-1895 the TOTAL FEE of $380.00 which covers the filing fee for this application. A duplicate copy of this sheet is enclosed.

4. _X_ The Assistant Commissioner is hereby authorized to charge payment of the following fees associated with this communication or credit any overpayment to Deposit Account No. 07-1895. A duplicate copy of this sheet is enclosed.

   _X_ Any additional filing fees required under 37 C.F.R. 1.16.
   _X_ Any patent application processing fees under 37 C.F.R. 1.17.

5. _X_ Amend the specification by inserting after the title on page 1:

This application is a divisional of application Serial No. _08/988,224, filed December 10, 1997, which is a divisional of U.S. Patent Application Serial No. 08/657,409, filed June 3, 1996, which is a continuation-in-part of U.S. Patent Application Serial No. 08/568,994, filed December 7, 1995 (now abandoned), which is a continuation-in-part of U.S. Patent Application Serial No. 08/503,606, filed July 18, 1995, the contents of which are incorporated by reference in their entirety herein.

6. _X_ A verified statement claiming small entity status was filed in parent application, Serial No. 08/657,409, filed on June 3, 1996, and such status is still proper.

7. _X_ The prior application is assigned of record to Diversa Corporation, on June 3, 1996, at Reel 8018, Frame 0180.

8. _X_ The power of attorney in the prior application is to Lisa A. Haile, Registration No. 38,347.

9. X Please transfer the drawings from the prior application to the new application.

10. X A copy of the prior application as filed is enclosed, including a copy of a Combined Declaration and Power of Attorney filed in parent application, U.S. application Serial No. 08/988,224, filed on December 10,1997.

11. __ Permission to Use Sequence Listing of parent priority is enclosed along with paper copy of Sequence Listing.

12. X Information Disclosure Statements filed in the prior application under 37 C.F.R. 1.97 are hereby made of record. Copy of PTO-1449 is enclosed.

Address all future communications to:

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The undersigned states that the enclosed application papers comprise a true copy of the prior application as filed.

Respectfully submitted,

Date: 10/19/99

Lisa A. Haile

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37 CFR 1.9(f) and 1.27(c) - SMALL BUSINESS CONCERN

I hereby declare that I am

[ ] the owner of the small business concern identified below:

[X] an official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF CONCERN: RECOMBINANT BIOCATALYSIS, INC.

ADDRESS OF CONCERN: 505 Coast Boulevard, 4th Floor, La Jolla, California 92037

I hereby declare that the above identified small business concern qualifies as a small business concern as defined in 13 CFR 121.3-18, and reproduced in 37 CFR 1.9(d), for purposes of paying reduced fees under Section 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the number of persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third-party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention entitled:

ENZYME ACTIVITY SCREENING OF CLONES HAVING DNA FROM UNCULTIVATED MICROORGANISMS

Inventors:
Jay Short; Barry Harris; Jeffrey L. Stein

described in:
[X] the specification filed herewith
[ ] application serial no. _____, filed _____
[ ] patent no. _____, issued _____

If the rights held by the small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below and no rights to the invention are held by any person, other than the inventor, who would not qualify as an independent inventor under 37 CFR 1.9(c) if that person made the invention, or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or as a nonprofit organization under 37 CFR 1.9(e).

NOTE: Separate verified statement are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

NAME: _____

ADDRESS: _____

[ ] Individual [ ] Small business [ ] Nonprofit organization

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

NAME OF PERSON SIGNING Jay M. Short

TITLE IN ORGANIZATION Chief Scientific Officer

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SIGNATURE Jay M. Short DATE 5/2/96

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Docket No. 331400-47

PROTEIN ACTIVITY SCREENING
OF CLONES HAVING DNA FROM UNCULTIVATED MICROORGANISMS

This application is a divisional application of U.S. Patent Application Serial No. 08/657,409, which was filed on June 3, 1996, which was a continuation-in-part of U.S. application Serial No. 08/568,994 which was filed on December 7, 1995 (copending) which is a continuation-in-part of U.S. application Serial No. 08/503,606 which was filed on July 18, 1995 (copending).

This invention relates to the field of preparing and screening libraries of clones containing microbially derived DNA.

Naturally occurring assemblages of microorganisms often encompass a bewildering array of physiological and metabolic diversity. In fact, it has been estimated that to date less than one percent of the world's organisms have been cultured. It has been suggested that a large fraction of this diversity thus far has been unrecognized due to difficulties in enriching and isolating microorganisms in pure culture. Therefore, it has been difficult or impossible to identify or isolate valuable proteins, e.g. enzymes, from these samples. These limitations suggest the need for altemative approaches to characterize the physiological and metabolic potential, i e. activities of interest of as-yet uncultivated microorganisms, which to date have been characterized solely by analyses of PCR amplified rRNA gene fragments, clonally recovered from mixed assemblage nucleic acids.

In one aspect, the invention provides a process of screening clones having DNA from an uncultivated microorganism for a specified protein, e.g. enzyme, activity which process comprises:

screening for a specified protein, e.g enzyme, activity in a library of clones prepared by

(i) recovering DNA from a DNA population derived from at least one uncultivated

microorganism; and

(ii) transforming a host with recovered DNA to produce a library of clones which are screened for the specified protein, e.g. enzyme, activity.

The library is produced from DNA which is recovered without culturing of an organism, particularly where the DNA is recovered from an environmental sample containing microorganisms which are not or cannot be cultured.

In a preferred embodiment DNA is ligated into a vector, particularly wherein the vector further comprises expression regulatory sequences which can control and regulate the production of a detectable proteins, e.g. enzyme, activity from the ligated DNA.

The f-factor (or fertility factor) in E. cold is a plasmid which effects high frequency transfer of itself during conjugation and less frequent transfer of the bacterial chromosome itself. To achieve and stably propogate large DNA fragments from mixed microbial samples, a particularly preferred embodiment is to use a cloning vector containing an f-factor origin of replication to generate genomic libraries that can be replicated with a high degree of fidelity. When integrated with DNA from a mixed uncultured environmental sample, this makes it possible to achieve large genomic fragments in the form of a stable "environmental DNA library."

In another preferred embodiment, double stranded DNA obtained from the uncultivated DNA population is selected by:

converting the double stranded genomic DNA into single stranded DNA;

recovering from the converted single stranded DNA single stranded DNA which specifically binds, such as by hybridization, to a probe DNA sequence; and

converting recovered single stranded DNA to double stranded DNA.

The probe may be directly or indirectly bound to a solid phase by which it is separated from single stranded DNA which is not hybridized or otherwise specifically bound to the probe.

The process can also include releasing single stranded DNA from said probe after recovering said hybridized or otherwise bound single stranded DNA and amplifying the single stranded DNA so released prior to converting it to double stranded DNA.

The invention also provides a process of screening clones having DNA from an uncultivated microorganisms for a specified protein, e.g en~yme, activity which comprises screening for a specified gene cluster protein product activity in the library of clones prepared by: (i) recovering DNA from a DNA population derived from at least one uncultivated microorganism; and (ii3 transforming a host with recovered DNA to produce a library of clones with the screens for the specified protein, e.g enzyme, activity. The library is produced from gene cluster DNA which is recovered without culturing of an organism, particularly where the DNA gene clusters are recovered from an envirorunental sample containing microorganisms which are not or cannot be cultured.

Alternatively, double-stranded gene cluster DNA obtained from the uncultivated DNA population is selected by converting the double-stranded genomic gene cluster DNA into single-stranded DNA; recovering from the converted single-stranded gene cluster polycistron DNA, single-stranded DNA which specifically binds, such as by hybridization, to a polynucleotide probe sequence; and converting recovered singlestranded gene cluster DNA to double-stranded DNA.

These and other aspects of the present invention are described with respect to particular preferred embodiments and will be apparent to those skilled in the art from the teachings herein.

The microorganisms from which the libraries may be prepared include prokaryotic microorganisms, such as Eubacteria and Archacbacteria, and lower eukaryotic microorganisms such as fungi, some algae and protozoa. The microorganisms are uncultured microorganisms obtained from environmental samples and such microorganisms may be extremophiles, such as thermophiles, hyperthermophiles, psychrophiles, psychrotrophs, etc.

As indicated above, the library is produced from DNA which is recovered without culturing of an organism, particularly where the DNA is recovered from an environmental sample containing microorganisms which are not or cannot be cultured. Sources of microorganism DNA as a starting material library from which DNA is obtained are particularly contemplated to include environmental samples, such as microbial samples obtained from Arctic and Antarctic ice, water or permafrost sources, materials of volcanic origin, materials from soil or plant sources in tropical areas. etc. Thus, for example, genomic DNA may be recovered from either uncultured or non-culturable organism and employed to produce an appropriate library of clones for subsequent determination of protein, e.g enzyme, activity.

Bacteria and many eukaryotes have a coordinated mechanism for regulating genes whose products are involved in related processes. The genes are clustered, in structures referred to as "gene clusters," on a single chromosome and are transcribed together under the control of a single regulatory sequence, including a single promoter which initiates transcription of the entire cluster. The gene cluster, the promoter, and additional sequences that function in regulation altogether are referred to as an "operon" and can include up to 20 or more genes, usually from 2 to 6 genes. Thus, a gene cluster is a group of adjacent genes that are either identical or related, usually as to their function.

Some gene families consist of identical members. Clustering is a prerequisite for maintaining identity between genes, although clustered genes are not necessarily identical. Gene clusters range from extremes where a duplication is generated to adjacent related genes to cases where hundreds of identical genes lie in a tandem array. Sometimes no significance is discemable in a repetition of a particular gene. A principal example of this is the expressed duplicate insulin genes in some species, whereas a single insulin gene is adequate in other mammalian species.

It is important to further research gene clusters and the extent to which the full length of the cluster is necessary for the expression of the proteins resulting therefrom. Further, gene clusters undergo continual reorganization and, thus, the ability to create heterogeneous libraries

of gene clusters from, for example, bacterial or other prokaryote sources is valuable in determining sources of novel proteins, particularly including proteins, e.g. enzymes, such as, for example, the polyketide syntheses that are responsible for the synthesis of polyketides having a vast array of useful activities. Other types of proteins that are the product(s) of gene clusters are also contemplated, including, for example, antibiotics, antivirals, antitumor agents and regulatory proteins, such as insulin.

Polyketides are molecules which are an extremely rich source of bioactivities, including antibiotics (such as tetracyclines and erythromycin), anti-cancer agents (daunomycin), immunosuppressants (FK506 and rapamycin), and veterinary products (monensin). Many polyketides (produced by polyketide syntheses) are valuable as therapeutic agents. Polyketide syntheses are multifunctional proteins, e.g. enzymes, that catalyze the biosynthesis of a hugh variety of carbon chains differing in length and patterns of functionality and cyclization. Polyketide synthase genes fall into gene clusters and at least one type (designated type I) of polyketide syntheses have large size genes and proteins, e.g. enzymes, complicating genetic manipulation and in v"ro studies of these genes/proteins.

The ability to select and combine desired components from a library of polyketides and postpolyketide biosynthesis genes for generation of novel polyketides for study is appealing. The method(s) of the present invention make it possible to and facilitate the cloning of novel polyketide syntheses, since one can generate gene banks with clones containing large inserts (especially when using the f-factor based vectors), which facilitates cloning of gene clusters.

Preferably, the gene cluster DNA is ligated into a vector, particularly wherein a vector further comprises expression regulatory sequences which can control and regulate the production of a detectable protein or protein-related array activity from the ligated gene clusters. Use of vectors which have an exceptionally large capacity for exogenous DNA introduction are particularly appropriate for use with such gene clusters and are described by way of example herein to include the f-factor (or fertility factor) of E. coli. This f-factor of E. cold is a plasmid which affect highfrequency transfer of itself during conjugation and is ideal to achieve and stably

propagate large DNA fragments, such as gene clusters frorr. mixed microbial samples.

The term "derived" or "isolated" means that material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide separated from some or all of the coexisting materials in the natural system, is isolated.

The DNA isolated or derived from these microorganisms can preferably be inserted into a vector prior to probing for selected DNA. Such vectors are preferably those containing expression regulatory sequences, including promoters, enhancers and the like. Such polynucleotides can bc part of a vector and/or a composition and still be isolated, in that such vector or composition is not part of its natural environment. Particularly preferred phage or plasmid and methods for introduction and packaging into them are described in detail in the protocol set forth herein.

The following outlines a general procedure for producing libraries from nonculturable organisms, which libraries can be probed to select therefrom DNA sequences which hybridize to specified probe DNA:

Obtain Biomass
DNA Isolation
Shear DNA (25 gauge needle)
Blunt DNA (Mung Bean Nuclease)
Methylate (EcoR I Methylase)
Ligate to EcoR I linkers (GGAATTCC)
Cut back linkers (EcoR I Restriction Endonuclease)
Size Fractionate (Sucrose Gradient)
Ligate to lambda vector (Lambda ZAP® (Stratagene) and gtl 1)
Package (in vitro lambda packaging extract)
Plate on E. cold host and amplify

The probe DNA used for selectively recovering DNA of interest from the DNA derived from the at least one uncultured microorganism can be a full-length coding region sequence or a partial coding region sequence of DNA for an protein, e.g. enzyme, of known activity, a phylogenetic marker or other identified DNA sequence. The original DNA library can be preferably probed using mixtures of probes comprising at least a portion of the DNA sequence encoding the specified activity. These probes or probe libraries are preferably single-stranded and the microbial DNA which is probed has preferably been converted into single-stranded form. The probes that are particularly suitable are those derived from DNA encoding proteins, e.g. enzymes, having an activity similar or identical to the specified protein, e.g enzyme, activity which is to be screened.

The probe DNA should be at least about 10 bases and preferably at least 15 bases. In one embodiment, the entire coding region may be employed as a probe. Conditions for the hybridization in which DNA is selectively isolated by the use of at least one DNA probe will be designed to provide a hybridization stringency of at least about 50% sequence identity, more particularly a stringency providing for a sequence identity of at least about 70%.

Hybridization techniques for probing a microbial DNA library to isolate DNA of potential interest are well known in the art and any of those which are described in the literature are suitable for use herein, particularly those which use a solid phasebound, directly or indirectly bound, probe DNA for ease in separation from the remainder of the DNA derived from the microorganisms.

Preferably the probe DNA is "labeled" with one partner of a specific binding pair (i.e. a ligand) and the other partner of the pair is bound to a solid matrix to provide ease of separation of target from its source. The ligand and specific binding partner can be selected from, in either orientation, the following: (1) an antigen or hapten and an antibody or specific binding fragment thereof; (2) biotin or iminobiotin and avidin or streptavidin; (3) a sugar and a lectin specific therefor; (4) a protein, e.g. enzyme, and an inhibitor therefor; (5) an apoenzyrne and cofactor; (6) complementary homopolymeric oligonucleotides; and (7) a hormone and a receptor therefor. The

solid phase is preferably selected from: (1) a glass or polymeric surface; (2) a packed column of polymeric beads: and (3) magnetic or paramagnetic particles.

The library of clones prepared as described above can be screened directly for enzymatic activity without the need for culture expansion, amplification or other supplementary procedures. However, in one preferred embodiment, it is considered desirable to amplify the DNA recovered from the individual clones such as by
PCR.

Further, it is optional but desirable to perform an amplification of the target DNA that has been isolated. In this embodiment the selectively isolated DNA is separated from the probe DNA after isolation. It is then amplified before being used to transform hosts. The double stranded DNA selected to include as at least a portion thereof a predetermined DNA sequence can be rendered single stranded, subjected to amplification and reannealed to provide amplified numbers of selected double stranded DNA. Numerous amplification methodologies are now well known in the art.

The selected DNA is then used for preparing a library for screening by transforming a suitable organism. Hosts, particularly those specifically identified herein as preferred, are transformed by artificial introduction of the vectors containing the target DNA by inoculation under conditions conducive for such transformation.

The resultant libraries of transformed clones are then screened for clones which display activity for the protein, e.g. enzyme, of interest in a phenotypic assay for protein, e.g. enzyme, activity.

Having prepared a multiplicity of clones from DNA selectively isolated from an organism, such clones are screened for a specific protein, e.g. enzyme, activity and to identify the clones having the specified protein, e.g enzyme, characteristics.

The screening for protein, e.g. enzyme, activity may be effected on individual expression clones or may be initially effected on a mixture of expression clones to ascertain whether or not the mixture has one or more specified protein, e.g. enzyme, activities. If the mixture has a specified protein, e.g. er~yme, activity, then the individual clones may be rescreened for such protein, e.g. enzyme, activity or for a more specific activity. Thus, for example, if a clone mixture has hydrolase activity, then the individual clones may be recovered and screened to determine which of such clones has hydrolase activity.

The DNA derived from a microorganism(s) is preferably inserted into an appropriate vector (generally a vector containing suitable regulatory sequences for effecting expression) prior to subjecting such DNA to a selection procedure to select and isolate therefrom DNA which hybridizes to DNA derived from DNA encoding an proteins, e.g. enzyme(s), having the specified protein, e.g. enzyme, activity.

As representative examples of expression vectors which may be used there may be mentioned viral particles, baculovirus, phage, plasmids, phagemids. cosmids, phosmids, bacterial artificial chromosomes, viral DNA (e.g. vaccinia, adenovirus, foul pox virus, pseudorabies and derivatives of SV40), Pl-based artificial chromosomes, yeast plasmids, yeast artificial chromosomes, and any other vectors specific for specific hosts of interest (such as bacillus, aspergillus, yeast, etc.) Thus, for example, the DNA may be included in any one of a variety of expression vectors for expressing a polypeptide. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences. Large numbers of suitable vectors are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example; Bacterial: pQE70, pQE60, pQE-9 (Qiagen), pBLUESCRIPT SK, pBLUESCRIPT KS (Stratagene); pTRC99a, pKK223-3, pDR540, pRIT2T (Pharmacia); Eukaryotic: pWLNEO, pXTI, pSG5 (Stratagene) pSVK3, pBPV, pMSG, pSVLSV40 (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.

A particularly preferred type of vector for use in the present invention contains an f-factor origin of replication. The f-factor (or fertility factor) in E. coli is a plasmid which effects high frequency transfer of itself during conjugation and less frequent transfer of the bacterial chromosome itself. A particularly preferred embodiment is to use cloning vectors, referred to as "fosmids" or bacterial artificial chromosome (BAC) vectors. These are derived from the E. cold f-factor and are able to stably integrate large segments of genomic DNA. When integrated with DNA from a mixed uncultured environmental sample, this makes it possible to achieve large genomic fragments in the form of a stable "environmental DNA library."

The DNA derived from a microorganism(s) may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Such procedures and others are deemed to be within the scope of those skilled in the art.

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. Particular named bacterial promoters include lacI, lacZ, T3, T7, apt, lambda PR, PL and trp. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40. LTRs from retrovirus, and mouse metallotnionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers.

In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in E. coli.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g, the ampicillin resistance gene of E. cold and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic proteins, e.g enzymes, such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium.

The DNA selected and isolated as hereinabove described is introduced into a suitable host to prepare a library which is screened for the desired protein, e.g. enzyme, activity. The selected DNA is preferably already in a vector which includes appropriate control sequences whereby selected DNA which encodes for an protein, e.g enzyme, may be expressed, for detection of the desired activity. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by transformation, calcium phosphate transfection, DEAE-Dextran mediated transfection, DMSO or electroporation (Davis, L., Dibner, M., Battey, I., Basic Methods in Molecular Biology, (1986)).

As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as E. coli, Bacillus, Streptomyces, Salmonella typhimurium; fungal cells, such as yeast; insect cells such as Drosophila S2 and Spodoptera SJ9; animal cells such as CHO, COS or Bowes melanoma; adenoviruses; plant cells, etc.

The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

Host cells are genetically engineered (transduced or transformed or transfected) w~th the vectors. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transfonnants or amplifying genes. The culture conditions. such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

The library may be screened for a specified protein, e.g. enzyme, activity by procedures known in the art. For example, the protein, e.g enzyme, activity may be screened for one or more of the six IUB classes; oxidoreductases, transferases, hydrolases, Iyases, isomerases and ligases. The recombinant proteins, e.g. enzymes, which are determined to be positive for one or more of the IUB classes may then be rescreened for a more specific protein, e.g. enzyme, activity.

Alternatively, the library may be screened for a more specialized protein, e.g enzyme, activity. For example, instead of generically screening for hydrolase activity, the library may be screened for a more specialized activity, i.e. the type of bond on which the hydrolase acts. Thus, for example, the library may be screened to ascertain those hydrolases which act on one or more specified chemical functionalities, such as: (a) amide (peptide bonds), i.e. proteases; (b) ester bonds, i.e. esterases and lipases; (c) acetals, i.e, glycosidases etc.

The clones which are identified as having the specified protein, e g. enzyme, activity may then be sequenced to identify the DNA sequence encoding an protein, e.g. enzyme, having the specified activity. Thus, in accordance with the present invention it is possible to isolate and identify: (i) DNA encoding an protein, e.g enzyme, having a specified protein, e.g. enzyme, activity, (ii) proteins, e.g. enzymes, having such activity (inlcuding the amino acid sequence thereof) and (iii) produce recombinant proteins, e.g. enzymes, having such activity.

The present invention may be employed for example, to identify uncultured microorganisms with proteins, e.g. enzymes, having, for example, the following activities which may be employed for the following uses:

1. Lipase/Esterase

   a. Enantioselective hydrolysis of esters (lipids)/ thioesters

      1) Resolution of racemic mixtures

      2) Synthesis of optically active acids or alcohols from mesodiesters

   b. Selective syntheses

      1) Regiospecific hydrolysis of carbohydrate esters

      2) Selective hydrolysis of cyclic secondary alcohols

   c. Synthesis of optically active esters, lactones, acids, alcohols

      1) Transesterification of activated/nonactivated esters

      2) Interesterification

      3) Optically active lactones from hydroxyesters

      4) Regio- and enantioselective ring opening of anhydrides

   d. Detergents

   e. Fat/Oil conversion

   f. Cheese ripening

2. Protease

   a. Ester/amide synthesis

   b. Peptide synthesis

   c. Resolution of racemic mixtures of amino acid esters

   d. Synthesis of non-natural amino acids

   e. Detergents/protein hydrolysis

3. Glycosidase/Glycosyl transferase

   a. Sugar/polymer synthesis

   b. Cleavage of glycosidic linkages to form mono, all-and oligosaccharides

   c. Synthesis of complex oligosaccharides

   d. Glycoside synthesis using UDP-galactosyl transferase

   e. Transglycosylation of disaccharides, glycosyl fluorides, aryl galactosides

   f. Glycosyl transfer in oligosaccharide synthesis

g. Diastereoselective cleavage of p-glucosylsulfoxides

h. Asyrnrnetric glycosylations

i. Food processing

j. Paper processing

4. Phosphatase/Kinase

a. Synthesis/hydrolysis of phosphate esters

1) Regio-, enantioselective phosphorylation

2) Introduction of phosphate esters

3) Synthesize phospholipid precursors

4) Controlled polynucleotide synthesis

b. Activate biological molecule

c. Selective phosphate bond formation without protecting groups

5. Mono/Dioxygenase

a. Direct oxyfunctionalization of unactivated organic substrates

b. Hydroxylation of alkane, aromatics, steroids

c. Epoxidation of alkenes

d. Enantioselective sulphoxidation

e. Regio- and stereoselective Bayer-Villiger oxidation

6. Haloperoxidase

a. Oxidative addition of halide ion to nucleophilic sites

b. Addition of hypohalous acids to olefinic bonds

c. Ring cleavage of cyclopropanes

d. Activated aromatic substrates converted to *ortho* and *para* derivatives

e. 1.3 diketones converted to 2-halo-derivatives

f. Heteroatom oxidation of sulfur and nitrogen containing substrates

g. Oxidation of enol acetates, alkynes and activated aromatic rings

7. Lignin peroxidase/Diarylpropane peroxidase

a. Oxidative cleavage of C-C bonds

b. Oxidation of benzylic alcohols to aldehydes

c Hydroxylation of benzylic carbons

d. Phenol dimerization

e. Hydroxylation of double bonds to form diols

f. Cleavage of lignin aldehydes

8. Epoxide hydrolase

a. Synthesis of enantiomerically pure bioactive compounds

b. Regio- and enantioselective hydrolysis of epoxide Aromatic and olefinic epaxidation by monoaxygenases to form epoxides

d. Resolution of racemic epoxides

e. Hydrolysis of steroid epoxides

9. Nitrile hydratase/nitriluse

a. Hydrolysis of aliphatic nitriles to carboxamides

b. Hydrolysis of aromatic, heterocyclic, unsaturated aliphatic nitriles to corresponding acids

c. Hydrolysis of acrylonitrile

d. Production of aromatic and carboxamides, carboxylic acids (nicotinamide, picolinarnide, isonicotinamide)

e. Regioselective hydrolysis of acrylic dinitrile

f. α-amino acids from a-hydroxynitriles

10. Transaminase

a. Transfer of amino groups into oxo-acids

11. Amidase/Acylase

a. Hydrolysis of amides, amidines, and other C-N bonds

b. Non-natural amino acid resolution and synthesis

Preparation of a Representative DNA Library

The following outlines the procedures used to generate a gene library from a sample of the exterior surface of a whale bone found at 1240 meters depth in the Santa Catalina Basin during a dive expedition.

Isolate DNA.

ISOQUICK Procedure as per manufacturer's instructions.

Shear DNA

1. Vigorously push and pull DNA through a 25G double-hub needle and l-cc syringes about 500 times.
2. Check a small amount (0.5 µg) on a 0.8% agarose gel to make sure the majority of the DNA is in the desired size range (about 3-6 kb).

Blunt DNA

1. Add:
   H_2O to a final volume of 405 µl
   45µl 10X Mung Bean Buffer
   2.0µl Mung Bean Nuclease (150 µ/µl)
2. Incubate 37°C, 15 minutes.
3. Phenol/chloroform extract once.
4. Chloroform extract once.
5. Add 1 ml ice cold ethanol to precipitate.
6. Place on ice for 10 minutes.
7. Spin in microfuge, high speed, 30 minutes.
8. Wash with 1 ml 70% ethanol.
9. Spin in microfuge, high speed, 10 minutes and dry.
   to a final volume of 4.0 µl

Methylate DNA

1. Gently resuspend DNA in 26 µl TE.
2. Add:

   4.0 µl 10X *EcoR* I Methylase Buffer

   0.5 µl SAM (32 mM)

   5.0 µl *EcoR* I Methylase (40 µ/µl)
3. Incubate 37°, 1 hour

Insure Blunt Ends

1. Add to the methylation reaction:

   5.0 µl 100 mM $MgCl_2$

   8.0 µl dNTP mix (2.5 mM of each dGTP, dATP, dTTP, dCTP)

   4.0 µl Klenow (5 µ/µl)
2. Incubate 12°C, 30 minutes.
3. Add 450 µl 1X STE.
4. Phenol/chloroform extract once.
5. Chloroform extract once.
6. Add 1 ml ice cold ethanol to precipitate and place on ice for 10 minutes.
7. Spin in microfuge, high speed, 30 minutes.
8. Wash with 1 ml 70% ethanol.
9. Spin in microfuge, high speed, lO minutes and dry.

Linker Ligation

1. Gently resuspend DNA in 7 µl Tris-EDTA (TE).
2. Add:

   14 µl Phosohorvlated *Eco*R I linkers (200 ng,/µl)

   3.0 µl 10X Litigation Buffer

   3.0 µl 10 mM rATP

   3.0 µl T4 DNA Ligase (4Wu/µl)
3. Incubate 4°C, overnight.

*EcoR*I Cutback

1. Heat kill ligation reaction 68°C, 10 minutes.
2. Add:

   237.9 H_20

   30 µl lOX *EcoR* I Buffer

   2.1 µl *EcoR* I Restriction Enzyme (100 u/µl)
3. Incubate 37°C, 1.5 hours.
4. Add 1.5 µl 0.5 M EDTA.
5. Place on ice.

Sucrose Gradient (2.2 ml) Size Fractionation

1. Heat sample to 65°C, 10 minutes.
2. Gently load on 2.2 ml sucrose gradient.
3. Spin in mini-ultracentrifuge, 45K, 20°C, 4 hours (no brake).
4. Collect fractions by puncturing the bottom of the gradient tube with a 20G needle and allowing the sucrose to flow through the needle. Collect the first 20 drops in a Falcon 2059 tube then collect lO 1-drop fractions (labelled 1-10). Each drop is about 60 µl in volume.
5. Run 5 µl of each fraction on a 0.8% agarose gel to check the size.
6. Pool fractions 1-4 (-10-1.5 kb) and, in a separate tube, pool fractions 5-7 (about 5-0.5 kb).
7. Add 1 ml ice cold ethanol to precipitate and place on ice for 10 minutes.
8. Spin in microfuge, high speed, 30 minutes.
9. Wash with 1 ml 70% ethanol.
10. Spin in microfuge, high speed, 10 minutes and dry.
11. Resuspend each in 10 µl TE buffer.

Test Ligation to Lambda Arms

1. Plate assay to get an approximate concentration. Spot 0.5 pl of the sample on agarose containing ethidium bromide along with standards (DNA samples of known concentration). View in UV light and estimate concentration compared to the standards.

   Fraction 1-4 = >1.0 µg/µl l. Fraction 5-7 = 500 ng/µl.

2. Prepare the following ligation reactions (5 pl reactions) and incubate 4°C, overnight:

Sample	H_2O	10X Ligase Buffer	10mM rATP	Lambda arms (gt11 and ZAP)	Insert DNA	T4 DNA Ligase (4 Wu/µ)
Fraction 1-4	0.5 µl	0.5 µl	0.5 µl	1.0 µl	2.0 µl	0.5 µl
Fraction 5-7	0.5 µl	0.5 µl	0.5 µl	1.0 µl	2.0 µl	0.5 µl

Test Package and Plate

1. Package the ligation reactions following manufacturer's protocol. Package 2.5 µl per packaging extract (2 extracts per ligation).
2. Stop packaging reactions with 500 µl SM buffer and pool packaging that came from the same ligation.
3. Titer 1.0 µl of each on appropriate host (OD6W = 1.0) [XLIBlue MRF for ZAP® (Stratagene) and Y1088 for gtl 1]

   Add 200 µl host (in mM $MgSO_4$) to Falcon 2059 tubes

   Inoculate with 1 µl packaged phage

   Incubate 37°C, 15 minutes

   Add about 3 ml 48°C top agar

   [50 ml stock containing 150 µl IPTG (0.5M) and 300 µl X-GAL (350 mg/ml)]

   Plate on 100mm plates and incubate 37°C, overnight.

4. Efficiency results:

gtll: 1.7×10^4 recombinants with 95% background

ZAP ® (Stratagene): 4.2×10^4 recombinants with 66% background

Contaminants in the DNA sample may have inhibited the enzymatic reactions, though the sucrose gradient and organic extractions may have removed them. Since the DNA sample was precious, an effort was made to "fix" the ends for cloning:

Re-Blunt DNA

1. Pool all left over DNA that was not ligated to the lambda arms (Fractions 1-7) and add H_2O to a final volume of 12 µl. Then add:
   - 143 µl H_2O
   - 20 µl 10X Buffer 2 (from Stratagene's cDNA Synthesis Kit)
   - 23 µl Blunting dNTP (from Stratagene's cDNA Synthesis Kit)
   - 2.0 µl Pfu (from Stratagene"s cDNA Synthesis
2. Incubate 72°C, 30 minutes.
3. Phenol/chloroform extract once.
4. Chloroform extract once.
5. Add 20 µL 3M NaOAc and 400 µl ice cold ethanol to precipitate.
6. Place at -20°C, overnight.
7. Spin in microfuge, high speed, 30 minutes.
8. Wash with 1 ml 70% ethanol.
9. Spin in microfuge, high speed, 10 minutes and dry.

(Do NOT Methylate DNA since it was already methylated in the first round of processing)

Adaptor Ligation

1. Gently resuspend DNA in 8 Ill EcoR I adaptors (from Stratagene's cDNA Synthesis Kit).
2. Add:

    1.0 µl 10X Ligation Buffer

    1.0 µl 10 mM rATP

    1.0 µl T4 DNA Ligase (4Wu/µl)
3. Incubate 4°C, 2 days.

(Do NOT cutback since using ADAPTORS this time. Instead, need to phosphorylate)

Phosphorylate Adaptors

1. Heat kill ligation reaction 70°C, 30 minutes.

    Add:

    1.0 µl 10X Ligation Buffer

    2.0 µl 10mM rATF

    6.0 µl H_2O

    1.0 µl PNK (from Stratagene's cDNA Synthesis Kit).
2. Incubate 37°C, 30 minutes.
3. Add 31 µl H_2O and 5 µl 10X STE.
4. Size fractionate on a Sephacryl S-500 spin column (pool fractuions 1-3).
5. Phenol/chloroform extract once.
6. Chloroform extract once.
7. Add ice cold ethanol to precipitate.
8. Place on ice, 10 minutes.
9. Spin in microfuge, high speed, 30 minutes.
10. Wash with 1 ml 70% ethanol.
11. Spin in microfuge, high speed, 10 minutes and dry.
12. Resuspend in 10.5 µl TE buffer.

Do not plate assay. Instead, ligate directly to arms as above escept use 2.5 µl of DNA and no water.

Package and titer as above.

Efficiency results:

gtll: 2.5 x 10^6 recombinants with 2.5% background

ZAP ® (Stratagene): 9.6 x 10^5 recombinants with 0% background

Amplification of Libraries (5.0 x 10^5 recombinants from each library)

1. Add 3.0 ml host cells (OD_{660}=1.0) to two 50 ml conical tube.
2. Inoculate with 2.5 X 10^5 pfu per conical tube.
3. Incubate 37°C, 20 minutes.
4. Add top agar to each tube to a final volume of 45 ml.
5. Plate the tube across five 150 mm plates.
6. Incubate 37°C, 6-8 hours or until plaques are about pin-head in size.
7. Overlay with 8-10 ml SM Buffer and place at 4°C overnight (with gentle rocking if possible).

Harvest Phage

1. Recover phage suspension by pouring the SM buffer off each plate into a 50-ml conical tube.
2. Add 3 ml chloroform, shake vigorously and incubate at room temperature, 15 minutes.
3. Centrifuge at 2K rpm, 10 minutes to remove cell debris.
4. Pour supernatant into a sterile flask, add 500 pl chloroform.
5. Store at 4°C.

Titer Amplified Library

1. Make serial dilutions:

   10^{-5} = 1 µl amplified phage in 1 ml SM Buffer

10^{-6} = 1 µl of the 10^{-3} dilution in 1 ml SM Buffer

2. Add 200 µl host (in 10 mM $MgSO_4$) to two tubes
3. Inoculate one with 10 µl 10^{-6} dilution (10^{-5}).
4. Inoculate the other with 1 µl 10^{-6} dilution (10^{-6}).
5. Incubate 37°C, 15 minutes.
6. Add about 3 ml 48°C top agar.

   [50 ml stock containing 150 µl 1PTG (0.5M) and 375 µl X-GAL (350 mg/ml)]
7. Plate on 100 mm plates and incubate 37°C, overnight
8. Results:

gtl 1:	1.7×10^{11}/ml
ZAP® (Stratagene):	2.0×10^{10}/ml

Example 2

Enzymatic Activity Assay

The following is a representative example of a procedure for screening an expression library prepared in accordance with Example 1. In the following, the chemical characteristic Tiers are as follows:

Tier 1: Hydrolase

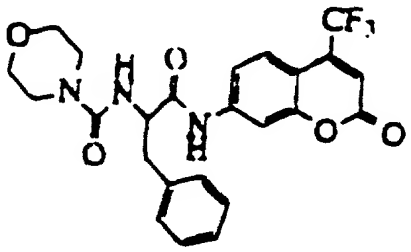
Tier 2: Amide, Ester and Acetal

Tier 3: Divisions and subdivisions are based upon the differences between individual substrates which are covalently attached to the functionality of Tier 2 undergoing reaction; as well as substrate specificity.

Tier 4: The two possible enantiomeric products which the protein, e.g. enzyme, may produce from a substrate.

Although the following example is specifically directed to the above mentioned tiers, the general procedures for testing for various chemical characteristics is generally applicable to substrates other than those specifically referred to in this Example.

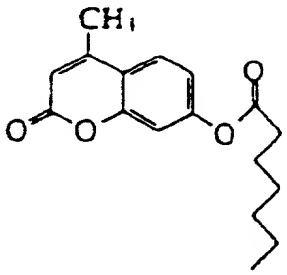
Screening for Tier 1-hydrolase; Tier 2-amide. Plates of the library prepared as described in Example 1 are used to multiply inoculate a single plate containing 200 µl of LB Amp/Meth, glycerol in each well. This step is performed using the High Density Replicating Tool (HDRT) of the Beckman Biomek with a 1% bleach, water, isopropanol, air-dry sterilization cycle between each inoculation. The single plate is grown for 2h at 37°C and is then used to inoculate two white 96-well Dynatech microtiter daughter plates containing 250 µl of LB Amp/Meth, glycerol in each well. The original single plate is incubated at 37°C for 18h, then stored at 80°C. The two condensed daughter plates are incubated at 37°C also for 18 h. The condensed daughter plates are then heated at 70°C for 45 min. to kill the cells and inactivate the host E.coli proteins, *e.g.* enzymes. A stock solution of 5mg/mL morphourea phenylalanyl-7-amino-4-trifluoromethyl coumarin (MuPheAFC, the 'substrate') in DMSO is diluted to 600 µM with 50 mM pH 7.5 Hepes buffer containing 0.6 mg/mL of the detergent dodecyl maltoside.



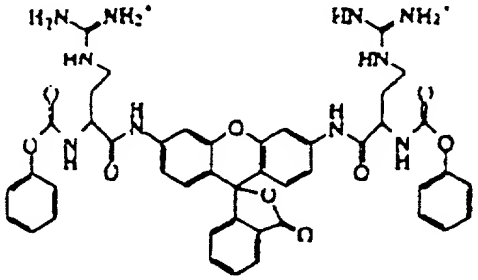
MuPheAFC

Fifty µL of the 600 µM MuPheAFC solution is added to each of the wells of the white condensed plates with one 100 µL mix cycle using the Biomek to yield a final concentration of substrate of ~100 µM. The fluorescence values are recorded (excitation = 400 nm, emission = 505 nm) on a plate reading fluorometer immediately after addition of the substrate (t=O). The plate is incubated at 70°C for 100 min, then allowed to cool to ambient temperature for 15 additional minutes. The fluorescence values are recorded again (t=100). The values at t=0 are subtracted from the values at t=l00 to determine if an active clone is present.

The data will indicate whether one of the clones in a particular well is hydrolyzing the substrate. In order to determine the individual clone which carries the activity, the source library plates are thawed and the individual clones are used to singly inoculate a new plate containing LB Amp/Meth. glycerol. As above, the plate is incubated at 37°C to grow the cells, heated at 70°C to inactivate the host proteins, *e.g.* enzymes, and 50 μL of 600 μM MuPheAFC is added using the Biomek. Additionally three other substrates are tested. They are methyl umbelliferone heptanoate, the CBZ-arginine rhodamine derivative, and fluorescein-conjugated casein (~3.2 mol fluorescein per mol of casein).



methyl umbelliferone heptanoate



(CBZ-arginine), rhodamine 110

The umbelliferone and rhodamine are added as 600 μM stock solutions in 50 μL of Hepes buffer. The fluorescein conjugated casein is also added in 50 μL at a stock concentration of 20 and 200 mg/mL. After addition of the substrates the t=0 fluorescence values are recorded, the plate is incubated at 70°C, and the t=100 min. values are recorded as above.

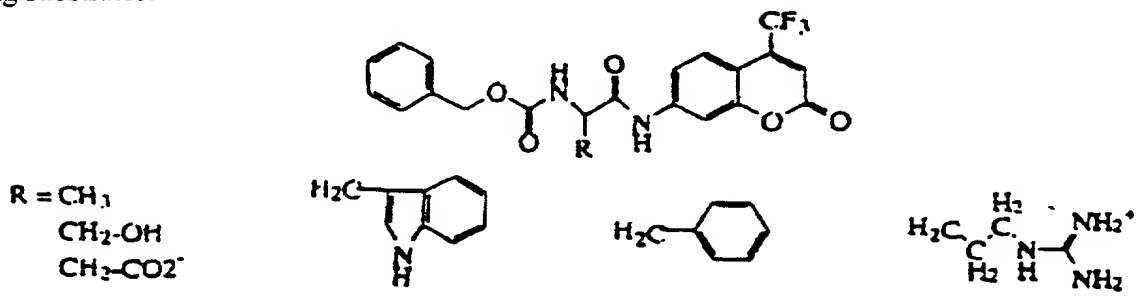
These data indicate which plate the active clone is in, where the arginine rhodamine derivative is also turned over by this activity, but the lipase substrate. methyl umbelliferone heptanoate, and protein, fluorescein-conjugated casein, do not function as substrates, the Tier I classification is 'hydrolase' and the Tier 2 classification is amide bond. No cross reactivity should be seen with the Tier 2-ester classification.

As shown in Figure 1, a recombinant clone from the library which has been characterized in Tier 1 as hydrolase and in Tier 2 as amide may then be tested in Tier 3 for various specificities. In Figure 1, the various classes of Tier 3 are followed by a parenthetical code which identifies the substrates of Table 1 which are used in identifying such specificities of Tier 3.

As shown in Figures 2 and 3, a recombinant clone from the library which has been characterized in Tier 1 as hydrolase and in Tier 2 as ester may then be tested in Tier 3 for various specificities. In Figures 2 and 3, the various classes of Tier 3 are followed by a parenthetical code which identifies the substrates of Tables 3 and 4 which are used in identifying such specificities of Tier 3. In Figures 2 and 3, R2 represents the alcohol portion of the ester and R' represents the acid portion of the ester.

As shown in Figure 4, a recombinanl clone from the library which has been characterized in Tier 1 as hydrolase and in Tier 2 as acetal may then be tested in Tier 3 for various specificities. In Figure 3, the various classes of Tier 3 are followed by a parenthetical code which identifies the substrates of Table 5 which are used in identifying such specificities of Tier 3.

Proteins, *e.g* enzymes, may be classified in Tier 4 for the chirality of the product(s) produced by the enzyme. For example, chiral amino esters may be determined using at least the following substrates:



For each substrate which is turned over the enantioselectivity value, E, is determined according to the equation below:

$$E = \frac{\ln[(1-c(1+ee_p)]}{\ln[(1-c(1-ee_p)]}$$

where ee_p = the enantiomeric excess (ee) of the hydrolyzed product and c = the percent conversion of the reaction. See Wong and Whitesides, Proteins, *e.g.* enzymes, in Synthetic Organic Chemistry, 1994, Elsevier, Tarrytown, New York, pp. 9-12.

The enantiomeric excess is determined by either chiral high performance liquid chromatography (HPLC) or chiral capillary electrophoresis (CE). Assays are performed as follows: two hundred pL of the appropriate buffer is added to each well of a 96-well white microtiter plate, followed by 50 μL of partially or completely purified protein, *e.g* enzyme, solution; 50 μL of substrate is added and the increase in fluorescence monitored versus time until 50% of the substrate is consumed or the reaction stops, whichever comes first.

Example 3

Construction of a Stable, Large Insert Picoplankton Genomic DNA Library

Figure 5 shows an overview of the procedures used to construct an environmental library from a mixed picoplankton sample. A stable, large insert DNA library representing picoplankton genomic DNA was prepared as follows.

Cell collection and preparation of DNA. Agarose plugs containing concentrated picoplankton cells were prepared from samples collected on an oceanographic cruise from Newport, Oregon to Honolulu, Hawaii. Seawater (30 liters) was collected in Niskin bottles, screened through 10 μm Nitex, and concentrated by hollow fiber filtration (Amicon DC10) through 30,000 MW cutoff polyfulfone filters. The concentrated bacterioplankton cells were collected on a 0.22 1lm, 47 mm Durapore filter, and resuspended in 1 ml of 2X STE buffer (1M NaCI, 0.1M EDTA, 10 mM Tris, pH 8.0) to a final density of approximately 1 x 10^{10} cells per ml. The cell suspension was mixed with one volume of 1% molten Seaplaque LMP agarose (FMC) cooled to 40°C, and then immediately drawn into a 1 ml syringe. The syringe was sealed with parafilm and placed on ice for 10 min. The cell-containing agarose plug was extruded into 10 ml of Lysis Buffer (lOmM Tris pH 8.0, 50 mM NaCI, 0.1M EDTA, 1% Sarkosyl, 0.2% sodium deoxycholate, 1 mg/ml lysozyme) and incubated at 37°C for one hour. The agarose plug was then transferred to 40 mls of ESP Buffer (1% Sarkosyl, 1 mg/ml proteinase K, in 0.5M EDTA), and incubated at 55°C for 16 hours. The solution was decanted and replaced with fresh ESP Buffer, and incubated at 55°C for an additional hour. The agarose plugs were then placed in

50 mM EDTA and stored at 4°C shipboard for the duration of the oceanographic cruise.

One slice of an agarose plug (72 µl) prepared from a sample collected off the Oregon coast was dialyzed overnight at 4°C against I mL of buffer A (1 00mM NaCI, 10mM Bis Tris Propane-HCI, 100 µg/ml acetylated BSA: pH 7.0 (@ 25°C) in a 2 mL microcentrifuge tube. The solution was replaced with 250 µl of fresh buffer A containing 10 mM $MgCl_2$ and 1 mM DTT and incubated on a rocking platform for 1 hr at room temperature. The solution was then changed to 250 µl of the same buffer containing 4U of Sau3A1 (NEB), equilibrated to 37°C in a water bath, and then incubated on a rocking platform in a 37°C incubator for 45 min. The plug was transferred to a 1.5 ml microcentrifuge tube and incubated at 68°C for 30 min to inactivate the protein, *e.g.* enzyme, and to melt the agarose. The agarose was digested and the DNA dephosphorylased using Gelase and HK-phosphatase (Epicentre), respectively, according to the manufacturer's recommendations. Protein was removed by gentle phenol/chloroform extraction and the DNA was ethanol precipitated, pelleted, and then washed with 70% ethanol. This partially digested DNA was resuspended in sterile H_2O to a concentration of 2.5 ng/µl for ligation to the pFOS1 vector.

PCR amplification results from several of the agarose plugs (data not shown) indicated the presence of significant amounts of archaeal DNA. Quantitative hybridization experiments using rRNA extracted from one sample, collected at 200 m of depth off the Oregon Coast, indicated that planktonic archaea in (this assemblage comprised approximately 4.7% of the total picoplankton biomass (this sample corresponds to "PACI"-200 m in Table 1 of DeLong *et al.*, high abundance of Archaea in Antarctic marine picoplankton, *Nature*, *371*:695-698, 1994). Results from archaeal-biased rDNA PCR amplification performed on agarose plug lysates confirmed the presence of relatively large amounts of archaeal DNA in this sample. Agarose plugs prepared from this picoplankton sample were chosen for subsequent fosmid library preparation. Each 1 ml agarose plug from this site contained approximately 7.5×10^5 cells, therefore approximately 5.4×10^5 cells were present in the 72 µl slice used in the preparation of the partially digested DNA.

Vector arms were prepared from pFOSI as described (Kim *et al.*, Stable propagation of casmid sized human DNA inserts in an F factor based vector, *Nucl. Acids Res., 20*:10832-10835, 1992). Briefly, the plasmid was completely digested with AstII, dephosphorylated with HK phosphatase, and then digested with BamHI to generate two anns, each of which contained a *cos* site in the proper orientation for cloning and packaging ligated DNA between 35-45 kbp. The partially digested picoplankton DNA, isolated by partial fragment gel electrophoresis (PFGE), was ligated ovemight to the PFOSI arms in a 15 µl ligation reaction containing 25 ng each of vector and insert and 1U of T4 DNA ligase (Boehringer-Mannheim). The ligated DNA in four microliters of this reaction was *in vitro* packaged using the Gigapack XL packaging system (Stratagene), the fosmid particles transfected to *E. coli* strain DH10B (BRL), and the cells spread onto LB_{cm15} plates. The resultant fosmid clones were picked into 96-well microliter dishes containing LB_{cm15} supplemented with 7% glycerol. Recombinant fosmids, each containing cat 40 kb of picoplankton DNA insert, yielded a library of 3,552 fosmid clones, containing approximately 1.4 x $1O^8$ base pairs of cloned DNA. All of the clones examined contained inserts ranging from 38 to 42 kbp. This library was stored frozen at -80°C for later analysis.

Numerous modifications and variations of the present invention are possible in light of the above teachings; therefore, within the scope of the claims, the invention may be practiced other than as particularly described.

Table 1

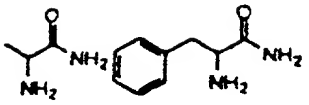
A2

Fluorescein conjugated casein (3.2 mol fluorescein/mol casein)

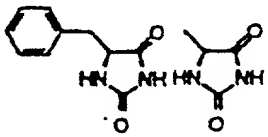
CBZ-Ala-AMC
t-BOC-Ala-Ala-Asp-AMC
succinyl-Ala-Gly-Leu-AMC
CBZ-Arg-AMC
CBZ-Met-AMC
morphourea-Phe-AMC

t-BOC = t-butoxy carbonyl, CBZ = carbonyl benzyloxy.
AMC = 7-amino-4-methyl coumarin

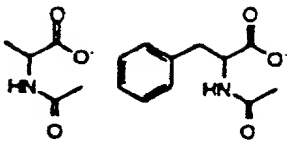
AA3



AB3



AC3



AD3

Fluorescein conjugated casein

t-BOC- Ala-Ala-Asp-AFC
CBZ- Ala-Ala-Lys-AFC
succinyl-Ala-Ala-Phe-AFC
succinyl-Ala-Gly-Leu-AFC

AFC = 7-amino-4-trifluoromethyl coumarin.)

AE3

Fluorescein conjugated casein

AF3

t-BOC- Ala-Ala-Asp-AFC
CBZ-Asp-AFC

AG3

CBZ- Ala-Ala-Lys-AFC
CBZ-Arg-AFC

AH3

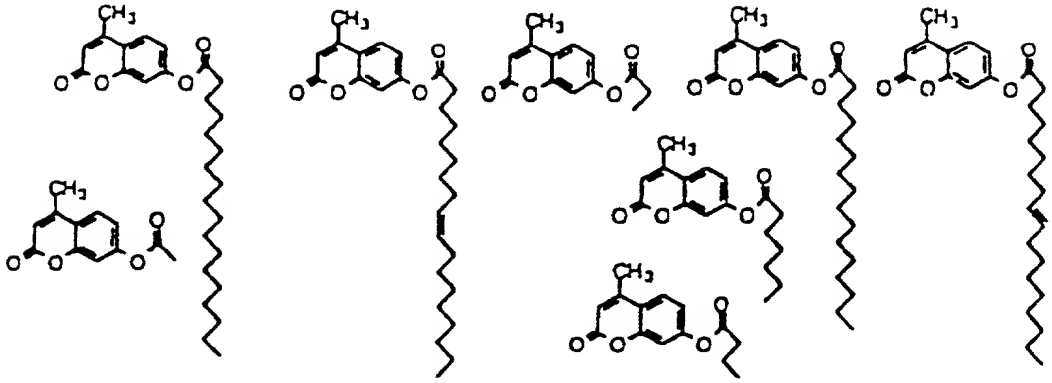
succinyl-Ala-Ala-Phe-AFC
CBZ-Phe-AFC
CBZ-Trp-AFC

AI3

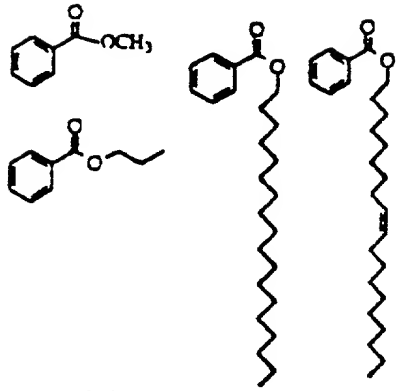
succinyl-Ala-Gly-Leu-AFC
CBZ-Ala-AFC
CBZ-Ser-AFC

Table 2

L2



LA3



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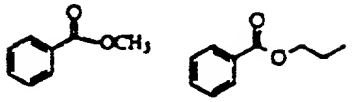

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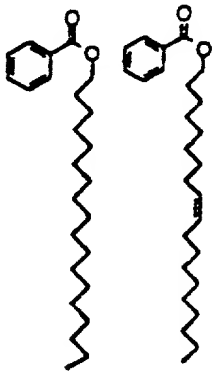

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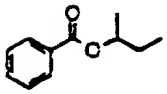
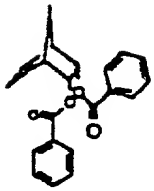


LF3



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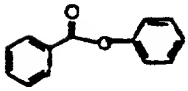
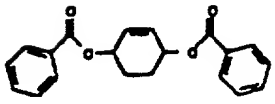


And all of L2

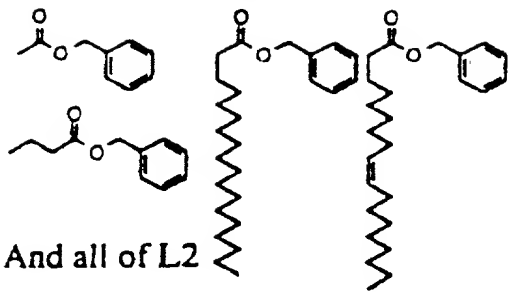
LG3



cis

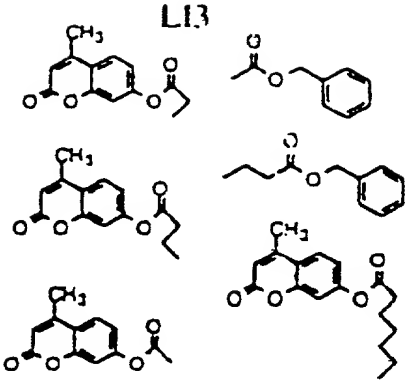
Table 3

LH3



And all of L2

LI3



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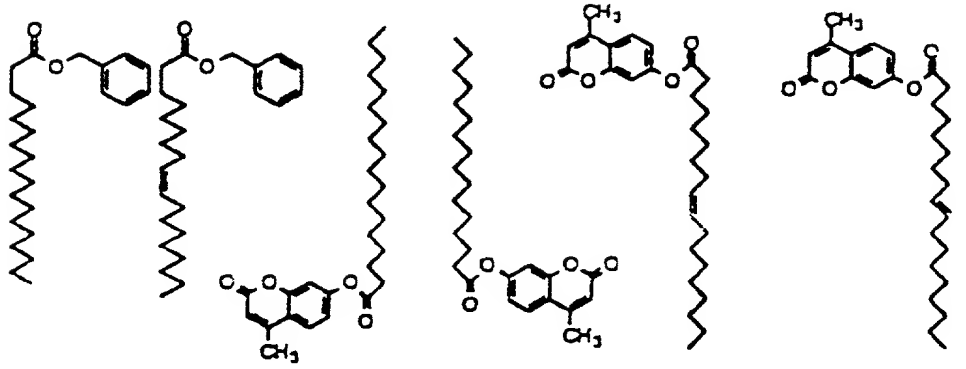

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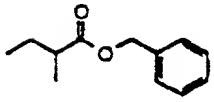

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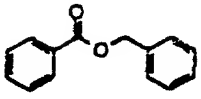

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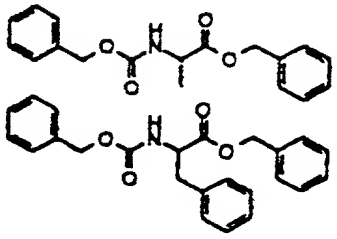

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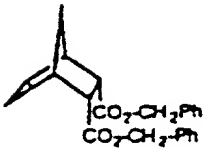


LO3

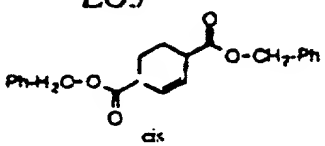
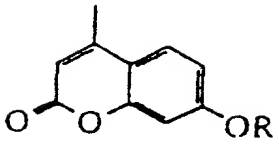


Table 4



4-methyl umbelliferone

wherein R=

G2	β-D-galactose
	β-D-glucose
	β-D-glucuronide
GB3	β-D-cellotrioside
	β-B-cellobiopyranoside
GC3	β-D-galactose
	α-D-galactose
GD3	β-D-glucose
	α-D-glucose
GE3	β-D-glucuronide
GI3	β-D-N,N-diacetylchitobiose
GJ3	β-D-fucose
	α-L-fucose
	β-L-fucose
GK3	β-D-mannose
	α-D-mannose

non-Umbelliferyl substrates

GA3	amylose [polyglucan α1,4 linkages], amylopectin [polyglucan branching α1,6 linkages]
GF3	xylan [poly 1,4-D-xylan]
GG3	amylopectin, pullulan
GH3	sucrose, fructofuranoside

WHAT IS CLAIMED IS:

1. A combinatorial gene expression library, comprising a pool of expression constructs, each expression construct containing one or more cDNA or genomic DNA fragments, wherein the cDNA or genomic DNA fragments in the pool of expression constructs are derived from a plurality of species of donor organisms, and wherein the cDNA or genomic DNA fragments in each expression construct are operably-associated each with one or more regulatory regions that drives expression of genes encoded by the cDNA or genomic DNA fragments in an appropriate host organism.

2. A method for making a combinatorial gene expression library, comprising ligating a DNA vector to one or more cDNA or genomic DNA fragments to generate a library of expression constructs, wherein the cDNA or genomic DNA fragments in the library of expression constructs are obtained from a plurality of species of donor organisms, and wherein genes contained in the cDNA or genomic DNA fragments are operably-associated with their native or exogenous regulatory regions which drive expression of the genes in an appropriate host cell.

3. A method for screening a gene expression library or a compound of interest, comprising:

(a) culturing the gene expression library of claim 1; and

(b) detecting a signal generated by the reporter regimen; thereby identifying a clone which produces the compound.

ABSTRACT

Disclosed is a process of screening clones having DNA from an uncultivated microorganism for a specified protein, *e.g.* enzyme, activity by screening for a specified protein, *e.g.* enzyme, activity in a library of clones prepared by (i) recovering DNA from a DNA population derived from at least one uncultivated microorganism; and (ii) transforming a host with recovered DNA to produce a library of clones which is screened for the specified protein, *e.g.* enzyme, activity.

Figure 2

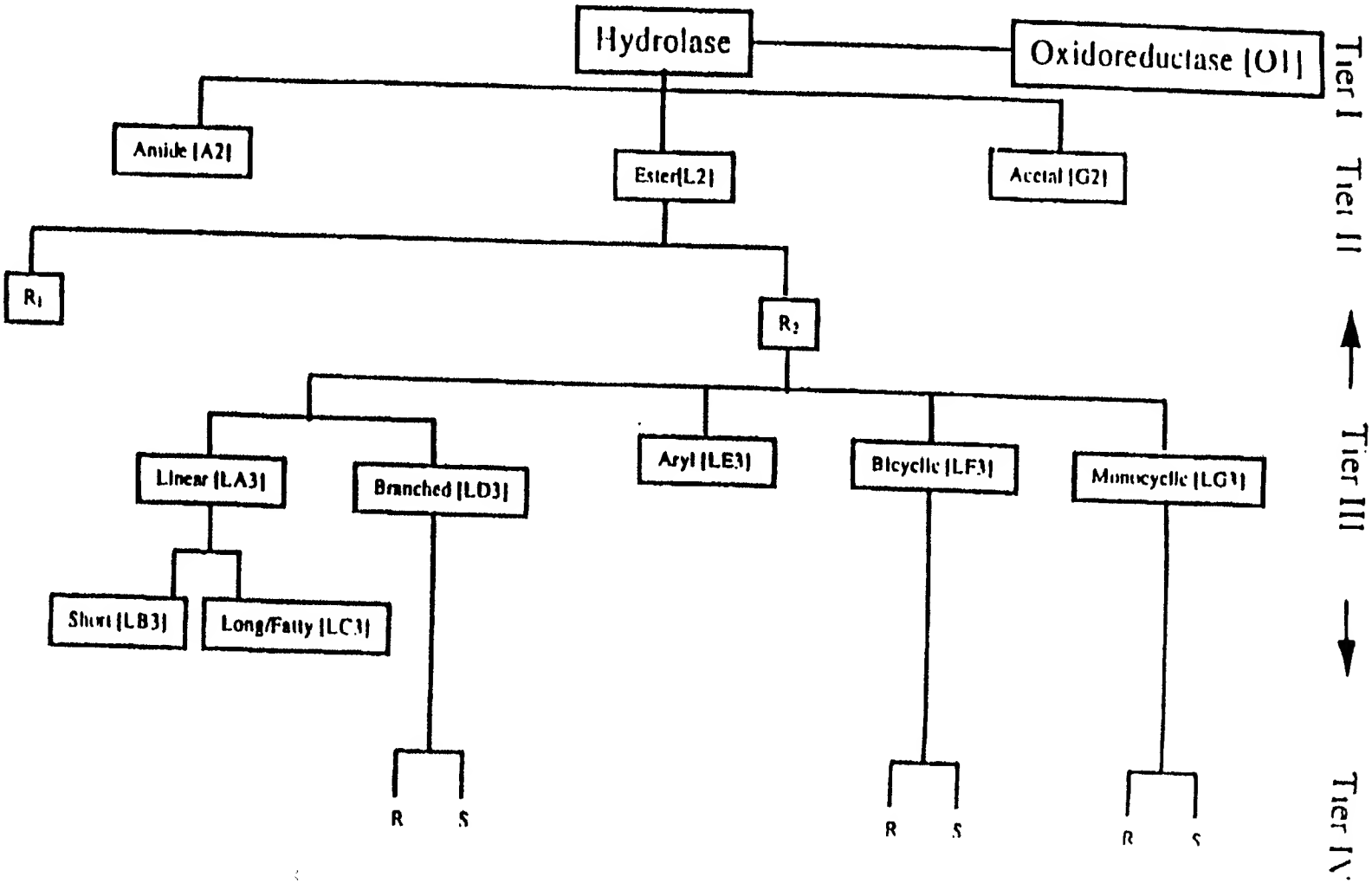

Hydrolase
Oxidoreductase [O1]
Amide [A2]
Ester[L2]
Acetal [G2]
R1
R2
Linear [LA3]
Branched [LD3]
Aryl [LE3]
Bicyclic [LF3]
Monocyclic [LG3]
Short [LB3]
Long/Fatty [LC3]
R
S
R
S
R
S
Tier I
Tier II
Tier III
Tier IV

Figure 3

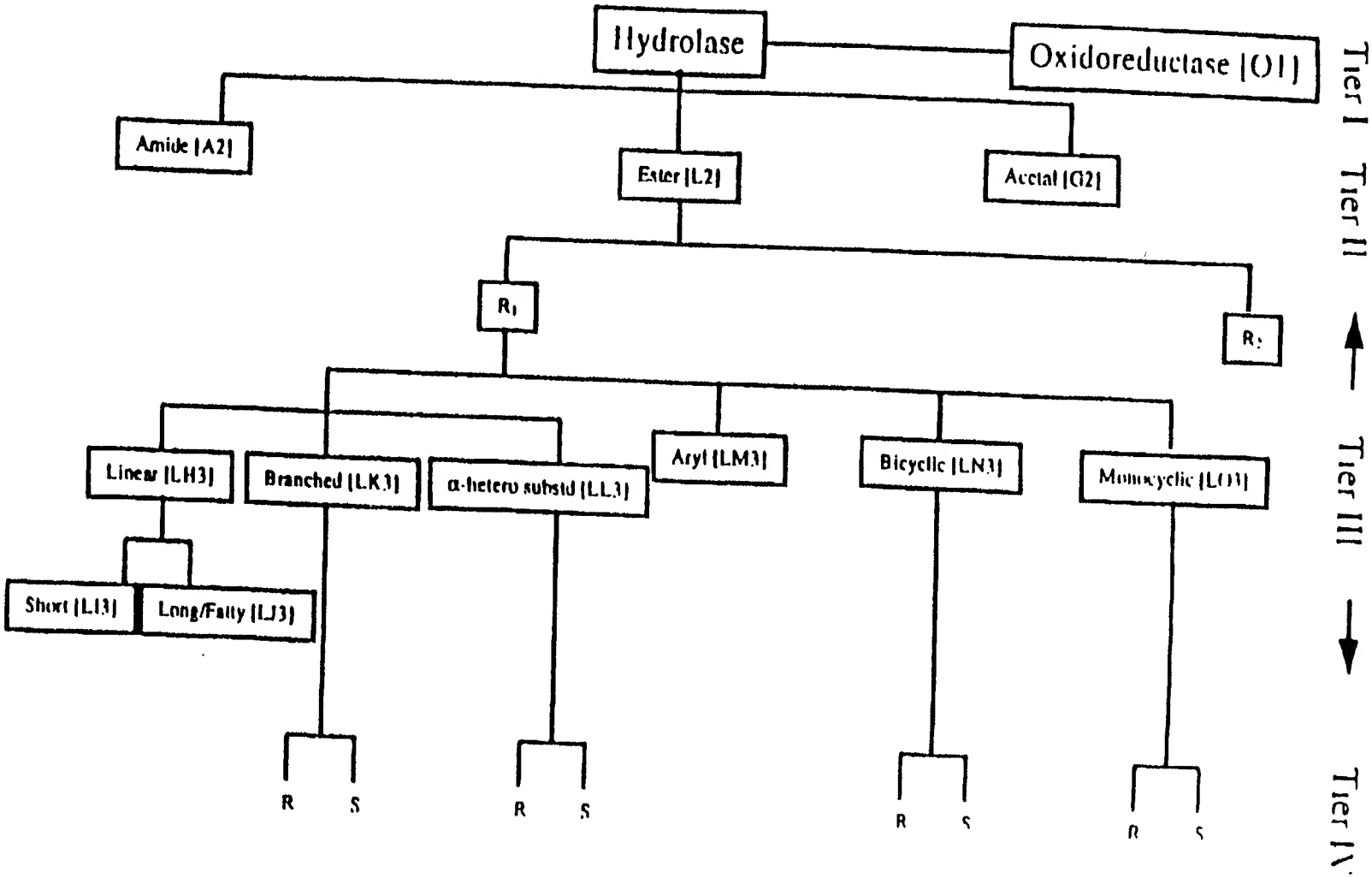


Figure 4

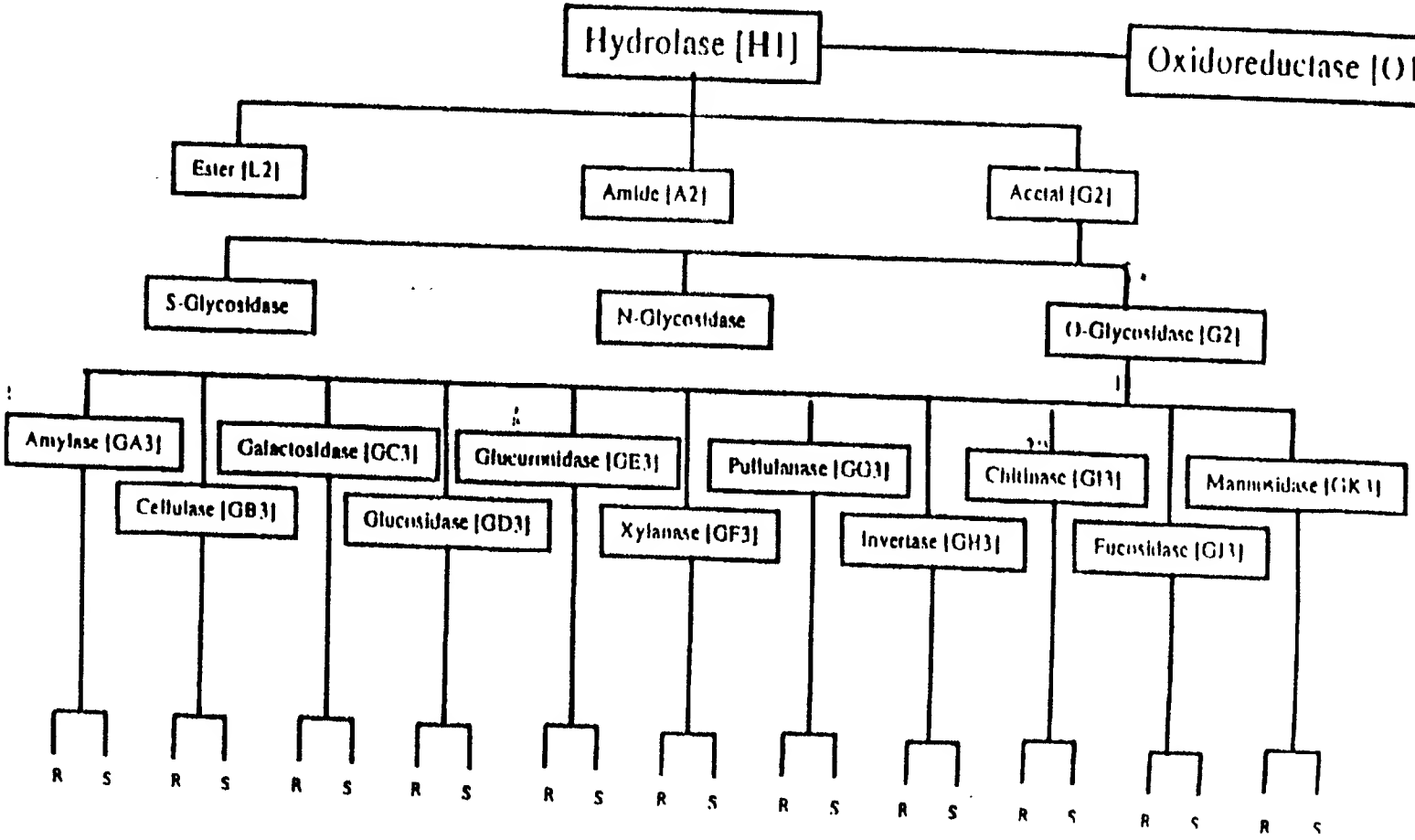
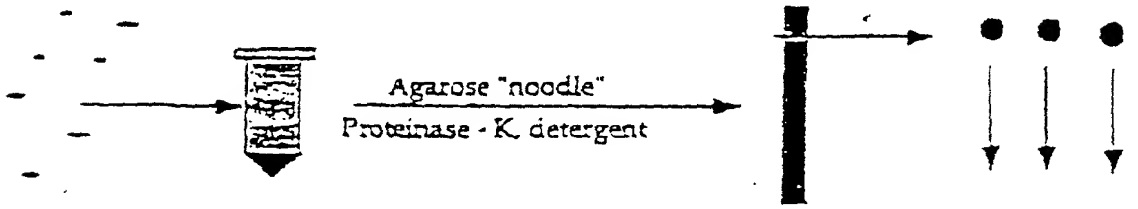


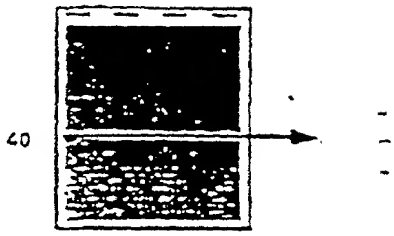
Figure 5

Environmental Library Construction in pFOS1

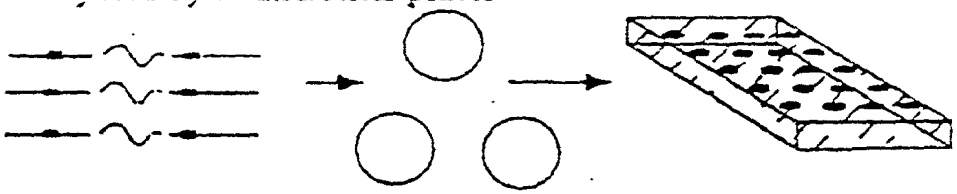
1. Concentrate bacteria, digest protein and preserve high MW DNA



2. Partially digest DNA and select 40 kbp fragments by PFGE or by λ-packaging (step 3)



3. Ligate to fosmid arms, package and transfect to *E. coli*. Array library in microtiter plates.



As a below named inventor, I hereby dec

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

ENZYME ACTIVITY SCREENING OF CLONES HAVING DNA FROM UNCULTIVATED MICROORGANISMS

the specification of which [X] is attached hereto or [ ] was filed on _____ as Application Serial No. _____ and was amended on _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above

I acknowledge the duty to disclose information which is material to the patentability of this application in accordance with Title 37, Code of Federal Regulations, Section 1.56(a).

I hereby claim foreign priority benefits under Title 35, United States Code, Section 119 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed. Prior Foreign Application(s):

			Priority Claimed
(Number)	(Country)	(Day/Month/Year Filed)	☐ ☐

I hereby claim the benefit under Title 35, United States Code, Section 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, Section 112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, Section 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

(Application Serial No.)	(Filing Date)	(Status - patented, pending, abandoned)

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith: John N. Bain (Reg. No. 18,651); John G. Gilfillan, III (Reg. No. 22,746); Elliot M. Olstein (Reg. No. 24,025); Raymond J. Lillie (Reg. No. 31,778); Charles J Herron (Reg. No. 28,019); William Squire (Reg. No. 25,378); and Gregory Ferraro (Reg. No. 36,134). Address correspondence and telephone calls to Charles J. Herron c/o Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein, 6 Becker Farm Road, Roseland, NJ 07068 - (201) 994-1700.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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Full name of third inventor: Jeffrey L. Stein

Inventor's signature: _____ Date: 5/16/96

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Post Office Address: same

Docket No. 331400-47

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